

Db 89 EGEREE 94

RESULT 2

ID 003865 PRELIMINARY; PRT; 582 AA.

AC 003865; 003865; PRELIMINARY; PRT; 582 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created) Best Local Similarity 36.2%; Pred. No. 1. 6e-03; Non_TER 238 AA; 27233 MW; FD31A80666738E68 CRC64; SQ

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE VILCIN-LIKE EMBRYO STORAGE PROTEIN.

GN GLOB1-L.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=W64A;

RX MEDLINE=92080707; PubMed=1752424;

RA Belanger F.C.; Kriz A.L.; Molecular basis for allelic polymorphism of the maize Globulin-1 gene.; X59033; CAA41809.1; -.

RL GENETICS 129:863-872(1991).

DR HSSP; P50477; ICAU.

DR MENDEL; 1134; Zeama;1188;11234.

DR INTERPRO; IPR00901; -.

DR INTERPRO; IPR00113; -.

DR PRODOM; PF00546; Seedstore_7s; 1.

DR PROSITE; PS00867; CPASE_2; UNKNOWN_1.

KW Seed Storage protein.

SEQUENCE 582 AA; 66162 MW; 680D85FEC07CB885 CRC64;

Query Match 36.1%; Score 138; DB 10; Length 582; Best Local Similarity 37.7%; Pred. No. 2e-08; Matches 26; Conservative 14; Mismatches 21; Indels 8; Gaps 3;

Qy 2 DDEDDRRGHSILOQCVCQRCRPRVSHARCVQECRQQ---QOGRHRHEEEQGRG 57

Db 26 DDNHHHHGGHKGSGCVRRC-EDRPHQRCLEOCREERERKQRSRHEADSGEG- 82

Qy 58 WHGEGEREE 66

SQ

Db 83 -SSEDEREQ 90

RESULT 4

ID 081249 PRELIMINARY; PRT; 238 AA.

AC 081249; 081249; PRELIMINARY; PRT; 238 AA.

DT 01-NOV-1998 (TREMBLrel. 08, Created) Best Local Similarity 35.6%; Score 136; DB 10; Length 238; Matches 25; Conservative 16; Mismatches 20; Indels 8; Gaps 3;

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE GLOBULIN-1 (FRAGMENT).

OS Zea mays subsp. mays (maize).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

OX NCBI_TaxID=4578;

RN [1]

RP SEQUENCE FROM N.A.

RA Hilton H.; Gaut B.S.; Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.; Genetics 0:0-0(1998).

RL GENETICS 0:0-0(1998).

DR EMBL; AF06412; AAC31455.1; -.

DR HSSP; P50477; ICAU.

DR MENDEL; 31891; Zeama;1188;31891.

DR INTERPRO; IPR00901; -.

DR INTERPRO; IPR00113; -.

DR PRODOM; PF00546; Seedstore_7s; 1.

DR PROSITE; PS00867; CPASE_2; UNKNOWN_1.

FT NON_TER 238 AA; 238 MW; EDF6A1DE3F86D0F0 CRC64;

SEQUENCE 238 AA; 27298 MW; EDF6A1DE3F86D0F0 CRC64;

Query Match 35.3%; Score 135; DB 10; Length 238; Best Local Similarity 36.2%; Pred. No. 2e-08; Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

Qy 2 DDEDDRRGHSILOQCVCQRCRPRVSHARCVQECRQQ---QOGRHRHEEEQGRG 57

Db 26 DDNHHHHGGHKGSGCVRRC-EDRPHQRCLEOCREERERKQRSRHEADSGKGS 84

Qy 58 WHGEGEREE 66

SQ

Db 85 -EDEREREQ 92

RESULT 5

ID 081255 PRELIMINARY; PRT; 238 AA.

AC 081255; 081255; PRELIMINARY; PRT; 238 AA.

DT 01-NOV-1998 (TREMBLrel. 08, Created) Best Local Similarity 36.2%; Pred. No. 1. 6e-03; Non_TER 238 AA; 27233 MW; FD31A80666738E68 CRC64; SQ

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DE GLOBULIN-1 (FRAGMENT).

OS Zea mays subsp. parviflumis.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

OX NCBI_TaxID=76912;

Qy 2 DDEDDRRGHSILOQCVCQRCRPRVSHARCVQECRQQ---QOGRHRHEEEQGRG 57

Db 26 DDNHHHHGGHKGSGCVRRC-EDRPHQRCLEOCREERERKQRSRHEADSGEG- 82

RN [1]
 RP SEQUENCE FROM N. A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives:
 evidence from the Globulin-1 gene.";
 RL Genetics 0:0-0(1998).
 DR EMBL; AF054224; ANC1467.1; -.
 DR MENDL; 31897; Zeana; 1180; 31897.
 DR INTERPRO; IPR001113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 DR NON_TER 238 AA; 238 MW; 1186EA5D6EEB507E CRC64;
 FT SEQUENCE 238 AA; 27205 MW; 1186EA5D6EEB507E CRC64;
 SQ

Query Match 35.3%; Score 135; DB 10; Length 238;
 Best Local Similarity 38.2%; Pred. No. 2e-08;
 Matches 26; Conservative 13; Mismatches 21; Indels 8; Gaps 3;
 QY 2 DDEDRRGHSLQQCVQRQERPRYSHARCVQCRDD---QQQHGRHEQQEEQGRGRG 57
 Db 26 DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLQCREERERKRSRHEADRSKGSS 84

QY 58 WHGGERE 65
 Db 83 -SSEDERE 89

RESULT 6
 Q9SB88 PRELIMINARY; PRT; 238 AA.
 ID Q9SB88
 AC Q9SB88;
 DT 01-MAY-2000 ("TREMBrel. 13, Created")
 DT 01-OCT-2000 ("TREMBrel. 13, Last sequence update")
 DT 01-OCT-2000 ("TREMBrel. 15, Last annotation update")
 DE GLOBULIN-1 (FRAGMENT)
 OS Zea mays subsp. parviflumis.
 OS Zea mays subsp. parviflumis.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea;
 NCBI_TAXID=76912; [1]
 RN SEQUENCE FROM N. A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives:
 evidence from the Globulin-1 gene.";
 RL Genetics 0:0-0(1998).
 DR EMBL; AF054221; AAC31464.1; -.
 DR HSSP; P50477; ICAU;
 DR INTERPRO; IPR00113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 FT SEQUENCE 238 AA; 27362 MW; A75C0C7DBD9B773A CRC64;
 SQ

Query Match 35.3%; Score 135; DB 10; Length 238;
 Best Local Similarity 36.2%; Pred. No. 2e-08;
 Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;
 QY 2 DDEDRRGHSLQQCVQRQERPRYSHARCVQCRDD---QQQHGRHEQQEEQGRGRG 57
 Db 26 DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLQCREERERKRSRHEADRSKGSS 84

QY 58 WHGGERE 66
 Db 85 -EDREREQ 92

RESULT 8
 Q9SB89 PRELIMINARY; PRT; 240 AA.
 ID Q9SB89
 AC Q9SB89;
 DT 01-MAY-2000 ("TREMBrel. 13, Created")
 DT 01-MAY-2000 ("TREMBrel. 13, Last sequence update")
 DT 01-OCT-2000 ("TREMBrel. 15, Last annotation update")
 DE GLOBULIN-1 (FRAGMENT)
 OS Zea mays subsp. parviflumis.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea;
 NCBI_TAXID=76912; [1]
 RN SEQUENCE FROM N. A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives:
 evidence from the Globulin-1 gene.";
 RL Genetics 0:0-0(1998).
 DR EMBL; AF054220; AAC31463.1; -.
 DR HSSP; P50477; ICAU;
 DR INTERPRO; IPR00113; -.
 DR PFAM; PF00546; Seedstore_7s; 1.
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 DR NON_TER 240 AA; 27492 MW; ECC26326633DFFB9 CRC64;
 FT SEQUENCE 240 AA; 27492 MW; ECC26326633DFFB9 CRC64;
 SQ

Query Match 35.3%; Score 135; DB 10; Length 240;
 Best Local Similarity 36.2%; Pred. No. 2.1e-08;
 Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;
 QY 2 DDEDRRGHSLQQCVQRQERPRYSHARCVQCRDD---QQQHGRHEQQEEQGRGRG 57
 Db 26 DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLQCREERERKRSRHEADRSKGSS 84

RESULT 7
 Q9SB80 PRELIMINARY; PRT; 240 AA.
 ID Q9SB80

DR HSSP; P50477; 1CAU
 DR INTERPRO; IPR000901; -
 DR INTERPRO; IPR01113; -
 DR PFAM; PF00546; Seedstore_7s; 1.
 DR PROSITE; PS0867; CPSASE_2; UNKNOWN_1.
 FT NON_TER 238 238
 SEQUENCE 238 AA; 27254 MW; FFEA7B7B4A25D68 CRC64;

Query Match 35.1%; Score 134; DB 10; Length 238;
 Best Local Similarity 36.2%; Pred. No. 2.7e-08;
 Matches 25; Conservative 15; Mismatches 21; Indels 8; Gaps 3;

Db 26 DDNHGGHKGKSGRCVRRC-EDRPHQPRCLEQCREERERKERSRHEADRSSEG- 82
 QY 58 WHGEGEREE 66
 Db 83 -SSEDEREQ 90

RESULT 13
 Q9S6Z6 PRELIMINARY; PRM; 238 AA.
 ID Q9S6Z6; PRM; 238 AA.
 AC 01-MAY-2000 (TREMBREL. 13, Created)
 DT 01-OCT-2000 (TREMBREL. 13, Last sequence update)
 DE GLOBULIN-1 (FRAGMENT).
 OS Zea luxurians (Teosinte).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 OC NCBI_TAXID=15945;
 RN 1
 RP SEQUENCE FROM N.A.
 RA Hilton H., Gaut B.S.;
 RT "Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.";
 RL Genetics 0:0-0(1998).
 EMBL; AF064232; AAC31475.1; -
 EMBL; AF064227; AAC31470.1; -
 EMBL; AF064230; AAC31473.1; -
 EMBL; P50477; 1CAU.
 DR INTERPRO; IPR000901; -
 DR INTERPRO; IPR001113; -
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 DR NCBI_TAXID=238
 FT SEQUENCE 238 AA; 27271 MW; FFE2169616319268 CRC64;

Query Match 35.1%; Score 134; DB 10;
 Best Local Similarity 36.2%; Pred. No. 2.7e-08;
 Matches 25; Conservative 15; Mismatches 21; Indels 8; Gaps 3;

Db 26 DDNHGGHKGKSGRCVRRC-EDRPHQPRCLEQCREERERKERSRHEADRSSEG- 82
 QY 58 WHGEGEREE 66
 Db 83 -SSEDEREQ 90

RESULT 14
 ID Q9S6Z6 PRELIMINARY; PRM; 238 AA.
 AC 01-NOV-1998 (TREMBREL. 08, Created)
 DT 01-OCT-2000 (TREMBREL. 08, Last sequence update)
 DE GLOBULIN-1 (FRAGMENT).
 DR HSSP; P50477; 1CAU.
 DR INTERPRO; IPR001113; -
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 DR NCBI_TAXID=240
 FT SEQUENCE 240 AA; 27560 MW; 5F54BC5CB06A983D CRC64;

Query Match 34.8%; Score 133; DB 10; Length 240;
 Best Local Similarity 36.2%; Pred. No. 3.5e-08;
 Matches 25; Conservative 15; Mismatches 23; Indels 6; Gaps 3;

Db 26 DDNHGGHKGKSGRCVRRC-EDRPHQPRCLEQCREERERKERSRHEADRSSEGSS 84
 QY 58 WHGEGEREE 66
 Db 85 -EDEREQ 92

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